CLAIMS

1. ~~Nucleic acid sequence, characterized in that it is~~ A nucleic acid comprising nucleic acids selected from the group consisting of:

- the sequence SEQ ID NO:1,

- the genomic sequences of variant erythroviruses, called erythrovirus type V9, which, molecularly, cannot be recognized as an erythrovirus B19 because it exhibits a genetic divergence ≥ 10% over the whole genome with respect to the erythrovirus B19 sequences and which exhibit a genetic divergence of less than or equal to 6% with respect to the sequence SEQ ID NO:1, and

- the erythrovirus genomic sequences capable of hybridizing under stringent conditions with one of the following sequences: SEQ ID NO:45-80, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119 and SEQ ID NO:120.

2. ~~Nucleic sequence according to~~ The nucleic acids of Claim 1, ~~characterized in that it has~~ wherein the nucleic acids exhibits a restriction profile according to Figures 7.1 to 7.3.

3. Fragments of ~~sequence SEQ ID NO:1~~ the nucleic acids, according to Claim 1, which are capable of allowing the detection of an erythrovirus V9, characterized in that they are selected from the group consisting of:

a) the sequences SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91 or SEQ ID NO:93,

b) the sequences SEQ ID NO:2-80

c) the sequences SEQ ID NO:105-121, and

d) the sequences complementary to the preceding sequences, ~~the fragments of~~ wherein the fragments comprise at least 17 nucleotides derived from the preceding sequences or their complementary sequences.

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4. ~~Fragment according to Claim 3, characterized in that it is~~ a fragment according to claim 3, selected from the group consisting of the sequences SEQ ID NO:45-80, 108 and NO: 110, their complementary sequences, the sequences of at least 17 nucleotides derived from these sequences and the sequences comprising the said sequences and ~~in that it~~ wherein the selected sequence is capable of serving as a probe in the specific identification of an erythrovirus V9 or of a related erythrovirus.

5. ~~Fragment according to Claim 3, characterized in that it is~~ a fragment according to Claim 3, selected from the group consisting of the sequences SEQ ID NO:2-80 and the sequences SEQ ID NO:105-121, their complementary sequences, the sequences of at least 17 nucleotides derived from these sequences and the sequences comprising the said sequences and ~~in that it is~~ wherein the selected sequence capable of serving as a primer for the amplification of sequences derived from an erythrovirus.

6. ~~Pairs~~ A pair of primers, characterized in that they are selected from the group consisting of:

- pair A: primers SEQ ID NO:111 and SEQ ID NO:112;
- pair B: primers SEQ ID NO:105 and SEQ ID NO:106;
- pair C: one of the sequences SEQ ID NO:2-44, 105, 106, 107, 109, 111 or 112 and one of the sequences SEQ ID NO:45-80, 108 or 110;
- pair D: primer SEQ ID NO:107 and primer SEQ ID NO:109;
- pair E: two primers selected from the sequences SEQ ID NO:2-44, 105, 106, 107, 109, 111 or 112; and
- pair F: two primers selected from the sequences SEQ ID NO:45-80, 108 or 110.

7. ~~Variant~~ A variant erythrovirus, characterized in that it cannot be recognized molecularly as an erythrovirus B19 genome, and in that it exhibits a genetic divergence of less than or equal to 6% with the sequence SEQ ID NO:1

and in that its genome hybridizes specifically, under stringent conditions with one of the sequences SEQ ID NO:45 to 80, 108 and 110.

8. ~~Plasmid~~ a plasmid, characterized in that it comprises the viral genome of a variant erythrovirus strain, called erythrovirus V9, which cannot be recognized molecularly as an erythrovirus B19 and which exhibits with the latter a genetic divergence of ≥ 10% over the whole genome with respect to the erythrovirus B19 sequences and a genetic divergence of less than or equal to 6% with the sequence SEQ ID NO:1 or a fragment thereof, according to Claim 3.

9. ~~Plasmid~~ a plasmid according to Claim 8, characterized in that it includes the sequence SEQ ID NO:1.

10. ~~Diagnostic~~ A diagnostic reagent for the differential detection of type V9 erythroviruses, characterized in that it is selected from the sequences SEQ ID NO:45-80, 108 and 110, their complementary sequences, and the sequences of at least 17 nucleotides, derived from these sequences, ~~optionally labelled with an appropriate marker~~.

11. ~~Method~~ A method for the rapid and differential diagnosis of erythroviruses, by hybridization and/or gene amplification, using a biological sample as starting material, which process is characterized in that it comprises:

(1) a step in which a biological sample to be analysed is brought into contact with at least one probe of sequence SEQ ID NO:45-80, 108 or 110, and

(2) a step in which the product(s) resulting from the erythrovirus nucleotide sequence-probe interaction is (are) detected by any appropriate means.

12. ~~Method~~ A method according to Claim 11, characterized in that it comprises, prior to step (1):

. a step of extracting of the nucleic acid to be detected, belonging to the virus genome, which may be present in the biological sample, and

. at least one gene amplification cycle.

13. ~~Method~~ according to Claim 12, characterized in that the amplification cycles are carried out with the aid of a pair of primers ~~according to Claim 6~~.

14. ~~Method~~ for the rapid and differential diagnosis of erythroviruses, characterized in that it comprises:

. a step of extracting of the nucleic acid to be detected, belonging to the virus genome, which may be present in the biological sample,

. at least one gene amplification cycle with the aid of a pair of primers according to Claim 6, and

. the detection of the amplified product, on the one hand, by hybridization with the sequence SEQ ID NO:121 and, on the other hand, by the action of the restriction enzyme MunI.

15. Use of the sequences according to any one of Claims 1 to 5, for carrying out a method of hybridization or of gene amplification of erythrovirus nucleic sequences, these methods being applicable to the *in vitro* diagnosis of the potential infection of an individual with an erythrovirus.

16. ~~Method~~ of screening and typing an erythrovirus V9 or a related virus, characterized in that it comprises bringing a probe selected from the group consisting of the sequences according to Claim 4, ~~optionally labelled~~, into contact with the nucleic acid of the virus to be typed, ~~optionally labelled~~, and detecting the nucleic acid-probe hybrid obtained.

17. ~~Products~~ of translation, characterized in that ~~they are~~ encoded by a nucleotide sequence according to Claim 1.

18. ~~Protein~~, characterized in that it is capable of being expressed with the aid of a nucleotide sequence according to Claim 1.

19. ~~Protein or peptide, characterized in that it is~~ derived from a variant erythrovirus type V9, as defined in Claim 1 and ~~in that it is~~ selected from the sequences:

a) SEQ ID NO:82 (NS1 protein), SEQ ID NO:86 (VP1 protein), SEQ ID NO:88 (single VP1 protein), SEQ ID NO:92 (VP2 protein) and SEQ ID NO:95-104, namely fragments of the VP1 protein [VP1a peptide (SEQ ID NO:95); VP1b peptide (SEQ ID NO:96); VP1c peptide (SEQ ID NO:97); peptide VP1d (SEQ ID NO:98); peptide VP1e (SEQ ID NO:99); peptide VP1f (SEQ ID NO:100)], or fragments of the VP2 protein [peptide VP2a (SEQ ID NO:101); peptide VP2b (SEQ ID NO:102); peptide VP2c (SEQ ID NO:103); peptide VP2d (SEQ ID NO:104)], and

b) the sequences derived from sequences a) comprising between 7 and 50 amino acids.

20. ~~Immunogenic compositions~~ an immunogenic composition comprising one or more products of translation of the nucleotide sequences according to Claim 17 ~~and/or one of the peptides or proteins according to Claim 18 or Claim 19~~.

21. ~~Antibodies~~ An antibody directed against one or more of the peptides or proteins according to ~~any one of Claims 17 to 20~~ Claim 17.

22. Method for the immunological detection of an erythrovirus V9 infection, characterized in that it comprises:

- for the detection of anti-erythrovirus V9 antibodies, bringing a biological sample into contact with a peptide according to any one of Claims 17 to 19 (serodiagnosis),

- for the detection of erythrovirus V9 viral proteins, bringing a biological sample into contact with an antibody according to Claim 21;

the reading of the result being revealed by an appropriate means, in particular EIA, ELISA, RIA, fluorescence.

23. Erythrovirus diagnostic kit, characterized in that it includes at least one reagent according to Claim 11 and/or a pair of primers according to Claim 6 and/or a peptide according to any one of Claims 17 to 19 and/or an antibody according to Claim 21.

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